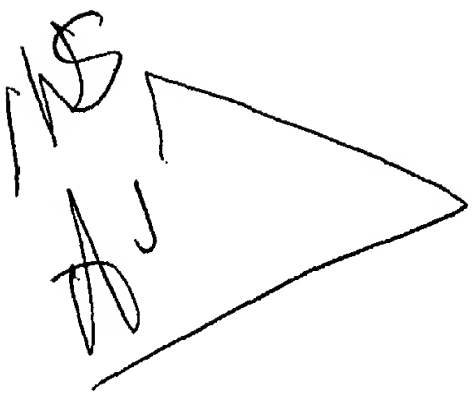

CLAIMS

The invention in which an exclusive right is asserted is claimed as follows:

1. A method for minimizing the aggregation tendencies of an amyloid forming protein, the method comprising:

a) identifying a first amino acid sequence of the protein that is replaced by a second amino acid sequence during physiological conditions; and

b) preventing the replacement by juxtaposing a peptide to the first amino acid sequence.

2. The method as recited in claim 1 wherein the method is conducted *in vivo*.

3. The method as recited in claim 1 wherein the protein is a human protein selected from the group consisting of human kappa-IV light chain variable domain and serine protease inhibitors.

4. The method as recited in claim 3 wherein the peptide has an amino acid sequence identical to an amino acid sequence in a region of the light chain variable domain.

5. The method as recited in claim 3 wherein the peptide is inserted between residue position numbers 60 and 83 of the protein.

6. The method as recited in claim 3 wherein the peptide has the amino acid sequence

Phe_{71}-Thr_{72}-Leu_{73}-Thr_{74}-Ile_{75}-Ser_{76}-Ser_{77}

and wherein the subscripts denote the positions of the amino acids in the domain.

7. The method as recited in claim 1 wherein the peptide is inserted when the protein is partially unfolded.

8. The method as recited in claim 1 wherein the peptide is identical in composition to a portion of the protein that anchors a hairpin-shaped amino acid sequence to the protein.

9. The method as recited in claim 1 wherein the protein is a greek key fold protein selected from the group consisting of antibody constant domains, transthyretin, beta-2-microglobulin, serine protease inhibitors, and crystalline.

10. The method as recited in claim 9 wherein the peptide is inserted at a hairpin anchorage point in the greek key fold protein.

11. The method as recited in claim 1 wherein the peptide is a target for an endoplasmic reticulum chaperone.

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12. The method as recited in claim 1 wherein the peptide is an endoplasmic reticulum chaperone selected from the group consisting of hsp70, hsc73 and BiP.

13. The method as recited in claim 1 wherein the peptide is a synthetic peptide selected from the group consisting of TDFTLTI, FTLTISS, FTLKISR, FTLEISR, and LTLKLSR.

14. A peptide for insertion in an intact human kappa-IV light chain variable domain, the peptide comprising the following amino acid sequence:

Phe_{71}-Thr_{72}-Leu_{73}-Thr_{74} -Ile_{75}-Ser_{76}-Ser_{77}

wherein the subscript numbers are the residue location points in the domain.

15. A method for preventing amyloid formation in human kappa-IV light chain variable domain, the method comprising inserting the peptide Phe_{71}-Thr_{72}-Leu_{73}-Thr_{74} -Ile_{75}-Ser_{76}-Ser_{77} into the domain, wherein the subscript numbers indicate the residue location on the domain.

16. The method as recited in claim 15 wherein the domain is partially unfolded at the time of insertion.

17. A method for preventing fibril assembly, the method comprising:

a) identifying a region of a first aggregating protein moiety that normally interacts with a second protein moiety to form the assembly; and

b) juxtaposing a binding protein to the first moiety.

18. The method as recited in claim 17 wherein the first and second aggregating proteins are immunoglobulin light chains.

19. The method as recited in claim 17 wherein the binding protein hybridizes with the region.

20. The method as recited in claim 17 wherein the binding protein is an amino acid sequence that is complementary to the amino acid sequence of the region.